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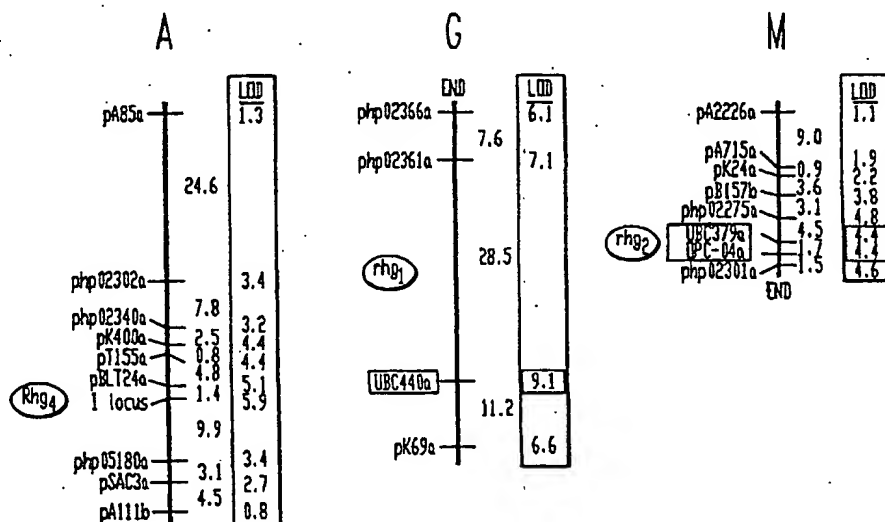


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(54) Title: SOYBEAN CYST NEMATODE RESISTANT SOYBEANS AND METHODS OF BREEDING AND IDENTIFYING RESISTANT PLANTS



(57) Abstract

A method for introgressing soybean cyst nematode resistance into elite soybean germplasm is disclosed. The method involves using genetically mapped loci associated with soybean cyst nematode resistance for marker-assisted selection during introgression of soybean cyst nematode resistance into elite soybean germplasm. Also disclosed are: a method for confirming selection for soybean cyst nematode resistance; quantitative trait loci associated with soybean cyst nematode resistance; and soybean lines bred to be resistant to soybean cyst nematode infestation.

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SOYBEAN CYST NEMATODE RESISTANT SOYBEANS
AND METHODS OF BREEDING AND IDENTIFYING
RESISTANT PLANTS

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FIELD OF THE INVENTION

This invention relates to soybeans and methods of soybean breeding. More particularly, the invention relates to soybean cyst nematode resistant soybean lines and methods of breeding same, the methods involving genetic marker analysis.

BACKGROUND OF THE INVENTION

Soybeans are a major cash crop and investment commodity in North America and elsewhere. Soybean oil is one of the most widely used edible oils, and soybeans are used worldwide both in animal feed and in human food production.

The soybean cyst nematode, Heterodera glycines Ichinohe, was first identified on soybeans in the United States in 1954 at Castle Hayne, North Carolina. Winstead, et al., Plant Dis. Rep. 39:9-11, 1955. Since its discovery the soybean cyst nematode ("SCN") has been recognized as one of the most destructive pests in soybean. It has been reported in nearly all states in which soybeans are grown, and it causes major production problems in several states, being particularly destructive in the midwestern states. See generally: Caldwell, et al., Agron. J. 52:635-636, 1960; Rao-Arelli and Anand, Crop. Sci. 28:650-652, 1988; Baltazar and Mansur, Soybean Genet. Newsl. 19:120-122, 1992; Concibido, et al., Crop. Sci., 1993. For example, susceptible soybean cultivars had 5.7-35.8% lower seed yields than did resistant cultivars on SCN race-3 infested sites in Iowa. Niblack and Norton, Plant Dis. 76:943-948, 1992.

Although the use of nematocides is effective in reducing the population level of the nematode, nematocide use is both uneconomical and potentially environmentally unsound as a control measure in soybean production.

Neither is crop rotation a practical means of nematode control, since rotation with a nonsusceptible crop for at least two years is necessary for reducing soybean losses. Therefore, it has long been felt by soybean breeders, that use of resistant varieties is the most practical control measure.

Screening of soybean germplasm for resistance to SCN was begun soon after the discovery of the nematode in the United States, and Golden, et al. (Plant Dis. Rep. 54:544-546, 1970) have described the determination of SCN races. Although SCN was discovered in North America about 40 years ago, soybean breeding for resistance to SCN has mostly utilized genes from two plant introductions -- Peking and PI88788, and while these lines have resistance genes for several SCN races, including race-3, they do not provide resistance to all known races.

The plant introduction PI437654 is the only known soybean to have resistance to SCN races-3 (Anand, Plant Dis. 68:593-595, 1984), 1, 2, 5, 14 (Anand, in Lambertin and Taylor (Eds), pp. 269-276, 1985), 6, and 9 (Rao-Arelli et al., Plant Dis. 76:894-896, 1992). However, PI437654 has black seed coat, poor standability, seed shattering, and low yield, necessitating the introgression of its SCN resistance into elite germplasm with a minimum of linkage drag. Conventional breeding with PI437654 produced the variety "Hartwig" (Anand, Crop Sci. 31:856, 1991), which is more adapted to cultivation and can be used as a source of SCN resistance in future soybean breeding.

Resistance to SCN is multigenic and quantitative in soybean (Mansur et al., Crop Sci. 1993), although complete resistance can be scored qualitatively. Myers and Anand (Euphytica 55:197-201, 1991) estimated that PI437654 has three genes required for complete resistance to SCN race-3, four genes for race-5, and three genes for race-14. The multiple genes and SCN races involved

contribute to the difficulty breeders have in developing SCN resistant soybean varieties.

Breeding programs for SCN resistance rely primarily on field evaluations where natural nematode populations occur. However, these populations can be mixtures of undetermined races (Young, Crop Sci. 22:385-388, 1982) and the environment can vary, thereby affecting the overwintering and infection capability of the nematodes (Niblack and Norton, Plant Dis. 76:943-948, 1992). Although evaluations using inbred nematode populations in controlled greenhouse environments are superior, they are prohibitively expensive, and the nematodes are difficult to manage for large breeding programs. These deficiencies in each evaluation method make SCN resistance a difficult trait for soybean improvement.

Genetic markers closely linked to important genes may be used to indirectly select for favorable alleles more efficiently than direct phenotypic selection (Lande and Thompson, Genetics 124:743-546, 1990). The i allele at the I locus, responsible for black or imperfect black seed-coat type, is closely linked in coupling to the SCN resistance allele, Rhg₄ in the variety Peking (Matson and Williams, Crop Sci. 5:477, 1965). The I locus was mapped to linkage group VII of the classical genetic map (Weiss, Crop. Sci. 10:627-629, 1970) and to linkage group A of the public RFLP map (Keim et al., Proc. 4th World Soy. Res. Conf., 1989). In addition, other SCN race-3 resistance loci have been associated with RFLP markers and tentatively mapped to linkage group B or G (Boutin et al., Soybean Genet. Newsl. 19:120-122, 1992) and possibly K (Concibido et al., Crop Sci., in press) using the germplasm source PI209332.

Therefore, it is of particular importance, both to the soybean breeder and to farmers who grow and sell soybeans as a cash crop, to identify, through genetic mapping, the quantitative trait loci (QTL) for resistance to the various SCN races. Knowing the QTLs associated with resistance to the SCN races, soybean breeders will

be better able to breed SCN resistant soybeans which also possess the other genotypic and phenotypic characteristics required for commercial soybean lines.

5 SUMMARY OF THE INVENTION

The present invention provides a method of introgressing SCN resistance into non-resistant soybean germplasm. Loci associated with SCN resistance in
10 soybean lines known to be resistant to SCN are used in marker assisted selection during introgression of SCN resistance into elite soybean germplasm. Examples of soybean lines known to be resistant to one or more races of SCN include PI437654, Peking, and PI90763. The method
15 of the present invention can be used to breed soybeans resistant to any SCN race. The SCN races of particular commercial importance are races-3, 1, 2, 5, 14, 6 and 9.

The method of the present invention comprises the use of nucleic acid markers genetically linked to loci
20 associated with SCN resistance in lines known to be resistant to one or more SCN races. The markers are used in genetic mapping of genetic material of soybean lines to be used in and/or which have been developed in a breeding program, allowing for marker-assisted selection
25 during introgression of SCN resistance into elite germplasm.

According to the method of the invention, any art-recognized genetic mapping techniques may be utilized, with preferred embodiments utilizing Restriction Fragment
30 Length Polymorphism (RFLP) mapping, RAPD mapping, or microsatellite mapping, using the nucleic acid markers recognized or applicable to the particular method(s). Markers useful in genetic mapping, and in a particular embodiment in RFLP mapping, include, for example, the
35 following: pA85a, php02302a, php02340a, pk400a, pt155a, pBLT24a, php05180a, pSAC3a, or pA111b for linkage group A; php02366a, php02361a, UBC440a, pK69a, or pL50b for linkage group G; and pA226a, pA715a, pk24a, pB157b,

php02275a, UBC379a, OPC-04a, or php02301a for linkage group M. Markers useful in the practice of the method of the present invention in an embodiment utilizing RAPD mapping include, for example, UBC440 for linkage group G and UBC379a and OPC-04a for linkage group M. An alternative embodiment of the present invention comprises a method of confirming selection for SCN resistance. This embodiment comprises identifying products of a soybean breeding program having in their genetic material the loci associated with resistance to one or more SCN races.

A further embodiment of the present invention comprises the quantitative trait loci (QTL) associated with SCN resistance. The loci of the invention are mapped (or identified or defined) using particular nucleic acid markers, as discussed above, and are further defined by their association with particular art-recognized linkage groups.

An additional embodiment of the present invention comprises soybeans resistant to the various SCN races bred according to the method of the present invention, or developed through the identification of parental lines possessing one or more of the QTL of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 shows RFLP and RAPD markers linked on SCN race-3 resistance loci. Groups A, G and M are presented, with RFLP and RAPD markers to the left of the groups (RAPD markers are enclosed in boxes). To the right of the group appear distances (in centimorgans) and LOD scores (enclosed in boxes).

FIGURE 2 presents a histogram correlating index of parasitism (as percent of cysts on the variety Essex) with marker classes at three resistance loci.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a novel and useful method for introgressing, in a reliable and predictable manner, SCN resistance into non-resistant soybean germplasm. The method involves the genetic mapping of loci associated with SCN resistance. SCN race resistance can be determined in any acceptable manner; preferably in greenhouse conditions using a homogeneous population of the particular SCN race.

The soybean line selected for mapping is subjected to DNA extraction. In a preferred embodiment the CTAB method (Murray and Thompson, Nucl. Acids Rev. 8:4321-4325, 1980; Keim et al., Soybean Genet. Newsl. 15:150-152, 1988) is used. Nucleic acid probes are used as markers in mapping the resistance loci, and appropriate probes are selected based upon the mapping method to be used. The probes can be either RNA or DNA probes, and mapping is performed using RFLP, RAPD, or microsatellite technology.

In a particular embodiment, DNA probes are used for RFLP markers. Such probes can come from, for example, Pst I-cloned genomic libraries, and the cloned inserts used as probes may be amplified, for example by PCR, LCR, NASBATM, or other amplification methods recognized in the art. For example, the markers useful in a preferred embodiment of the invention include the following: pA85a, php02302a, php02340a, pk400a, pt155a, pBLT24a, php05180a, pSAC3a, or pA111b for linkage group A; php02366a, php02361a, UBC440a, pK69a, or pL50b for linkage group G; and pA226a, pA715a, pk24a, pB157b, php02275a, UBC379a, OPC-04a, or php02301a for linkage group M. Of course it will be apparent to those skilled in the art that other markers which map to loci for SCN resistance may be utilized in the practice of the invention. For RFLP mapping, restriction fragments are generated using specific restriction enzymes, and the digestion, electrophoresis, Southern transfers and

nucleic acid hybridizations are conducted according to art-recognized techniques. See, e.g., Keim et al., Theor. Appl. Genet. 77:786-792, 1989, the disclosures of which are hereby incorporated herein by reference.

5 In an alternative embodiment of the method of the invention, RAPD technology can be utilized for genetic mapping. A DNA preparation is amplified using art-recognized amplification techniques, and suitable nucleic acid markers are used; for example, UBC440 for linkage
10 Group G and UBC379a and OPC-04a for linkage Group M.

In a soybean breeding program, the method of the present invention envisions the use of marker-associated selection for one or more loci at any stage of population development in a two-parent population, multiple parent
15 population, or a backcross population. Such populations are described in Fehr, W.R. 1987, Breeding Methods for Cultivar Development, in J.R. Wilcox (ed.) Soybeans: Improvement, Production, and Uses, 2d ed., the disclosures of which are hereby incorporated herein by
20 reference.

Marker-assisted selection according to art-recognized methods may be made, for example, step-wise, whereby the different SCN resistance loci are selected in more than one generation; or, as an alternative example,
25 simultaneously, whereby all three loci are selected in the same generation. Marker-assisted selection for SCN resistance may be done before, in conjunction with, or after testing and selection for other traits such as seed yield.

30 The DNA from target populations may be obtained from any plant part, and each DNA sample may represent the genotype of single or multiple plant individuals (including seed).

Marker-assisted selection may also be used to
35 confirm previous selection for SCN race-3 resistance or susceptibility made by challenging plants with soybean cyst nematodes in the field or greenhouse and scoring the resulting phenotypes.

The following examples are offered by way of illustration and not by way of limitation.

Example 1

Identification of SCN Race 3 Resistance Loci

5

Materials and Methods

Germplasm Development and Characteristics

A population of 328 recombinant-inbred lines (RILs) was licensed by Pioneer Hi-Bred International, Inc. from Iowa State University and used in this study. This population originated from a cross between two soybean max lines, PI437654 and BSR101, and was developed by single-seed-descent inbreeding from the F₂ to the F₆:7 generation (Baltazar and Mansur, Soybean Genet. News1. 19:120-122, 1992; Keim et al., Crop. Sci., in press). PI437654 is a plant introduction from China in the USDA soybean germplasm collection received from the USSR in 1980 (Nelson et al, USDA-ARS Tech. Bull. 1726, 1988). It is in Maturity Group III and resistant to all known races of SCN. BSR 101 was developed at Iowa State University and is in Maturity Group I and susceptible to SCN (Tachibana et al., Crop Sci. 27:612, 1987). At the I locus, PI437654 carries the i allele for black or imperfect black seed, and BSR101 carries the iⁱ allele for yellow or green seed. The RIL population was scored for these alleles and the I locus was mapped as a marker.

25

Soybean-Cyst-Nematode Screening

SCN race-3 resistance screening was conducted in a greenhouse using a homogeneous field population of SCN race-3 obtained from the Ames Plantation, near Grand Junction, TN (courtesy of Dr. L.D. Young, USDA-ARS, Jackson, TN). This race-3 isolate was increased and maintained for approximately 60 generations on roots of the standard susceptible cultivar, Essex, in a greenhouse at the Delta Center, University of Missouri, Portageville. In standardized host trials, it averaged 3, 1, 4, 4, and 186 white females (cysts) per plant on

35

Peking, PI90763, PI88788, Picket 71, and Essex, respectively.

Ten plants from each of 298 F_{6:7} RILs of the PI437654 X BSR101 population were evaluated against SCN race-3 in batches of 30 RILs and the five host differentials. The inoculation and evaluation methods were as previously described (Rao-Arelli and Anand, Crop Sci. 28:650-652, 1988; Rao-Arelli et al., Plant Dis. 75:594-595, 1991). Thirty days after inoculation, plant roots were washed and dislodged white females were counted under a stereomicroscope. Index of Parasitism (IP) was calculated for each RIL as a percentage of the cysts on Essex using the formula:

$$\text{IP} = \frac{\text{Avg. No. of cysts per RIL}}{\text{Avg. No. of cysts per Essex (susceptible)}} \times 100$$

Laboratory Methods

The DNA of soybean material was extracted using the CTAB method (Murray and Thompson, Nucl. Acids Rev. 8:4321-4325, 1980; Keim et al., Soybean Genet. Newsl. 15:150-152, 1988), with the following modifications. The lyophilized tissue was powdered by adding 2.5g of glass beads (Fisher cat. #11-312A) and 750mg of tissue in a 50mL tube and shaking in a paint-can shaker. The concentration of CTAB (hexadecyltrimethyl-ammonium bromide) in the extraction and precipitation buffers was reduced from 1% to 0.5%. After the DNA was precipitated with CTAB, the DNA pellet was dissolved in 2mL 1M NaCl with shaking at 65°C, 200 rpm, for 2-3 hr. The DNA was re-precipitated by adding 4.5mL ice cold 95% EtOH. The spooled DNA was washed with 1mL of 65%, then 1mL of 85% EtOH, to further remove salts. After the EtOH washes, the DNA was dissolved in 500-1000uL TE (10,1) and stored at 4°C until used.

The DNA probes used for RFLP markers came from PstI-cloned genomic libraries as described by Keim and Shoemaker (Soybean Genet. Newsl. 15:147-148, 1988) and cDNA libraries (U.S.D.A.-A.R.S., Beltsville, MD). The

cloned inserts used as probes were amplified by the polymerase chain reaction. Oligonucleotides of the T₃ and T₇ promoter regions of the phagemid vector pBS⁺/- were used as amplification primers. The restriction enzymes EcoRI, HindIII, EcoRV, DraI, TaqI, and HaeIII were used to digest the parental and population DNA. Six hundred sixty-three RFLP markers were used against PI437654 and BSR101 to identify and map 306 RFLP markers segregating in the RIL population. The DNA digestions, electrophoresis, Southern transfers, and DNA hybridizations were conducted as previously described (Keim et al., Theor. Appl. Genet. 77:786-792, 1989).

Statistical analyses

An analysis of variance for the IP from 10 replications (single plants) and 298 treatments (RILs) was used to calculate a broad-sense heritability estimate for resistance using the formula:

$$\text{Heritability} = \frac{\text{MS}_{\text{entry}} - \text{MS}_{\text{error}}}{\text{MS}_{\text{entry}}}$$

where MS_{entry} is the mean square of RILs and MS_{error} is the mean square of residual error.

Genetic linkages and distances between markers were estimated by maximum likelihood analysis of segregating RFLP-marker patterns in the RIL population, using the computer program MAPMAKER/EXP 3.0 (Lincoln et al., Whitehead Inst. Biomed. Res., 1993). A maximum likelihood test was conducted at each marker position to identify those markers significantly (LOD > 3.0) associated with phenotypic variation in SCN race-3 reaction using the computer program MAPMAKER/QT1 (Lincoln and Lander, Whitehead Inst. Biomed. Res., 1990). Because this population was inbred, having a high degree of homozygosity, only additive genetic effects were estimated.

Results

Heritability

The broad-sense heritability determination of 0.97 for IP indicated the number of cysts per plant within inbred lines was highly consistent. With heritability high, non-genetic variation was well controlled and genetic loci contributing to phenotypic variation could be more accurately detected with markers.

Locations of three SCN race-3 resistance loci

Three independent marker loci, the I locus, php02361a, and php02275a, had LOD scores greater than 3.0 for association with SCN race-3 resistance. These markers were located on RFLP linkage groups A, G, and M, respectively (Fig.1). We estimated the approximate map positions for resistance quantitative-trait-loci (QTL) based on the size of marker-QTL LOD scores and the distances between markers. The resistance QTL on G and M were each clearly placed between two markers because those markers had the highest LOD scores on those groups. However, the resistance QTL on A could not be clearly placed between the I locus and an adjacent marker because, though pBLT24a had the second highest LOD score on that group, the QTL could be on either side of the I locus and still be closer to pBLT24a than to php05180a (Fig. 1).

Level of resistance

Fifty-five of the 298 lines had complete resistance (IP < 2%) to SCN race-3. Eleven more lines had IP scores of 5-10%, but these lines did not carry resistance alleles at all three loci (indicated by flanking-marker scores) so were not counted as resistant. This is contrary to a commonly used classification system where resistance is defined as an IP less than 10% (Golden et al., Plant Dis. Rep. 54:544-546, 1970).

Thirty-eight resistant lines were expected in this inbred population provided three genes were needed and had normal (1:1) segregation ratios. This difference from the expected had a chi square (χ^2) of 7.6,

significant at $P < 0.01$. Most markers in this experiment had equivalent numbers of alleles from each parent (data not shown). However, either by chance or natural or unintentional selection, the markers around the resistance locus on M had approximately twice as many alleles from PI437654 as from BSR101. This alone can explain the higher number of expected resistant lines. Assuming PI437654 allele frequencies of 0.5, 0.5, and 0.67 at the resistance loci on A, G, and M, respectively, we would expect 50 resistant lines, which is not significantly different ($\chi^2 = 0.5$, $P < 0.01$) than the 55 found.

The genetic interval between QTL-flanking markers on G (php02361a to pK69a) was 39.7cM, compared to 11.3cM on A (pBLT24a to php05180a) and 7.7cM on M (php02275a and php02301a) (Fig. 1). Despite this increased interval, both markers flanking the resistance locus on G had higher LOD scores for marker-trait associations than did any markers on A and M. The detection of a QTL effect by marker analysis is a function of both the QTL expression and the distance between QTL and markers. Having higher LOD scores at markers on G despite more recombination between the resistance locus and markers, indicates the locus on G has greater effect on SCN resistance than the resistance loci on A and M. Also, the average IP score for the ABA genotypic class, carrying a resistance allele (B) only at the locus on G, was less than for the classes BAA and AAB, where a resistance allele is carried only on A or M, respectively (Fig. 2).

Lines having a resistance allele only on A or M had approximately the same number of cysts as lines having no resistance alleles at any loci, and lines having resistance alleles at any two of the three loci averaged fewer cysts than lines having resistance alleles at one or no loci (Fig. 2). Partial resistance seems to be attributable to the resistance locus on G and to any combination of resistance alleles at two of the three loci.

Complete, or nearly complete, resistance to SCN race-3 was obtained in all 21 lines having the PI437654 marker-type (B) at the six RFLP markers flanking the three loci (Table 1). These same 21 lines had either
5 black or imperfect-black seed-coat types, requiring the i allele at the I locus; thus the i allele was closely linked in coupling to the Rhg₄ resistance allele.

TABLE 1

Index of parasitism scores and seed-coat type of
 PI437654 X BSR101 recombinant-inbred lines having the
 5 PI437654 marker score (B) at six RFLP markers flanking
 the SCN race-3 resistance loci mapped to linkage groups
 A, G, and M

Line	IP (%) ^a	Seed Type ^b	Marker Score					
			A		G		M	
			pBLT24a	php 05180a	php 02361a	php pK69a	php 02275a	php 2301a
3	1.1	ibl	B	B	B	B	B	B
10	0.0	bl	B	B	B	B	B	B
22	0.6	ibl	B	B	B	B	B	B
66	0.0	ibl	B	B	B	B	B	B
79	0.0	bl	B	B	B	B	B	B
93	0.0	bl	B	B	B	B	B	B
96	0.0	bl	B	B	B	B	B	B
114	0.0	ibl	B	B	B	B	B	B
125	0.5	ibl	B	B	B	B	B	B
128	0.0	bl	B	B	B	B	B	B
130	0.5	bl	B	B	B	B	B	B
178	0.0	bl	B	B	B	B	B	B
193	0.6	bl	B	B	B	B	B	B
202	0.6	bl	B	B	B	B	B	B
203	0.0	bl	B	B	B	B	B	B
214	0.0	ibl	B	B	B	B	B	B
218	0.6	bl	B	B	B	B	B	B
221	0.0	bl	B	B	B	B	B	B
265	0.9	bl	B	B	B	B	B	B
271	0.0	ibl	B	B	B	B	B	B
299	1.1	ibl	B	B	B	B	B	B

^a IP < 2% considered completely resistant

^b bl = black; ibl = imperfect black

Nomenclature of SCN race-3 loci

Three independent loci necessary for complete resistance to SCN race-3 were genetically mapped in the soybean PI437654. Myers and Anand (Euphytica 55:197-201, 1991) found four of 48 F₃ families from the cross PI437654 X Essex resistant to SCN race-3, a proportion that approximates a three-gene system. In that same study, the segregation ratio of F₂ plants indicated one locus was dominant and two loci were recessive. The soybean varieties Peking and PI90763 also have one dominant and two recessive resistance loci for SCN race-3, (Rao-Arelli et al., Crop. Sci. 32:862-846, 1992). All progeny from crosses between Peking, PI90763, and PI437654 are resistant to SCN race-3; therefore, the SCN race-3 resistance alleles in these three varieties are at the same three loci (Rao-Arelli and Anand, Crop. Sci. 28:650-652, 1988; Myers and Anand, Euphytica 55:197-201, 1991; Rao-Arelli et al., Crop. Sci. 32:862-864, 1992).

Matson and Williams (Crop Sci. 5:477, 1965) reported a dominant SCN resistance locus, they named Rhg₄, about 0.35 recombination units from the I locus was the closest marker associated with a resistance locus on linkage group A (LOD score 5.9, Fig. 1). We assigned Rhg₄ to this resistance locus on our map because Peking and PI437654 have the same three SCN race-3 resistance loci and in each variety one locus is dominant. We could not confirm the gene action of any resistance loci because the population we used was inbred; however, given the overall similarity between SCN race-3 resistance in both PI437654 and Peking, we believe Rhg₄ is the dominant locus in PI437654.

Caldwell et al., (Agron. J. 52:635-636, 1960) identified three recessive loci, rhg₁, rhg₂, and rhg₃, in Peking for SCN race-1 resistance. Later, Rao-Arelli et al., (_____ 1992) assigned rhg₁ and rhg₂ to the two recessive loci for SCN race-3 resistance found in Peking, and selected rhg₂ to be the recessive resistance locus also found in the soybean PI88788. Because different SCN

5 races were used, the rhg₁ and rhg₂ designations may have been assigned to different loci in each study. It is unknown whether the same two loci govern both SCN race-1 and race-3 resistance. We have added genetic map
10 information to the identification of the two resistance loci found on G and M in PI437654 and Peking. We propose that the locus on G be rhg₁ and the locus on M be rhg₂. As more map data becomes available for different sources of SCN resistance and different SCN races, the map
15 locations and locus names assigned here can be referenced to determine when loci are in common and when to name new loci.

Comparison to previous RFLP mapping studies

15 Many of the RFLP markers in this study have been used by others, and some have been previously associated with the I locus and SCN race-3 resistance. Keim et al., (1990) linked pT153 (pT153 equals pT155 in band pattern and two map locations) and pA111 to the I locus. Our genetic distances between these markers and the I locus
20 were comparable to theirs.

Using PI209332 as the source of SCN resistance, Concibido et al., (Crop Sci., in press) found pA85 on group A significantly associated with SCN race-3 resistance, while pA111 on the same group was not. Our
25 results with these two markers were similar, with pA85 having a higher LOD score than pA111 (Fig. 1). However, pA85a on our map was 41.9cM from the I locus compared with the 10.9cM found by Concibido et al. We placed five additional markers between pA85 and the I locus, of which
30 pBLT24 was the nearest RFLP marker to Rhg₄.

Boutin, et al., (Soybean Genet. Newsl. 19:123-127, 1992) and later Concibido, et al. (Crop Sci., in press) reported pK69 on either linkage group B or G associated with SCN race-3 resistance in PI209332. We show that
35 this marker is associated with a resistance locus on group G (Fig. 1). pK69 had been an end marker of group G (formerly linkage group D, Diers, et al. (Theor. Appl. Genet. 83:608-612, 1992)), and we found rhg₁ outside this

linkage group of markers. We placed two new RFLP markers beyond pK69 and rhg₁, thereby marking rhg₁ from both sides (Fig. 1).

Concibido, et al. (Crop Sci., in press) also reported the marker pB32 associated with SCN race-3 resistance in PI209332, but were unsure of the linkage group. It is believed pB32 can hybridize to four loci, two of which were mapped in these experiments to linkage groups J and K and were not associated with SCN race-3 resistance. They may have used one of the other two possible marker-loci for this probe. Their pB32 marker was linked to a pK417 marker, which was less significantly associated with SCN resistance. pK417 markers have been mapped to lineage groups A, K, and M on the USDA/Iowa State University public RFLP map. We did not use pK417, but comparing our map with the ISU public map, the pK417 markers on both A and M appear near enough to possibly detect linkage to the SCN resistance loci on either of those groups. PI209332 may have a different mode of SCN race-3 resistance than PI437654. Rao-Arelli, et al. (Agronomy Abstracts, 1993) reported that the SCN race-3 resistance in PI209332 is likely controlled by two loci, one dominant and one recessive. If so, evidence from Concibido, et al. (Crop Sci., in press) indicates those two loci are on linkage groups A and G, and the pB32 marker used by them would therefore go to group A.

Marker-assisted selection

The markers used in these experiments, or similarly placed markers, on groups A, G, and M can be used for marker-assisted selection of SCN race-3 resistance in soybean breeding. In this population, 21 lines have the PI437654 marker type at six markers flanking the three resistance loci, and all have virtually complete resistance to SCN race-3 (Table 1). However, all 21 lines also have black or imperfect black seed coat types which are undesirable for breeding. The linkage between the I locus and Rhg₄ has been broken and Rhg₄ moved into adapted germplasm, most recently with the release of the

variety Hartwig which has both PI437654 and Peking in its pedigree (Anand, Crop Sci. 31:856, 1991). Though three loci would provide complete resistance to SCN race-3, partial resistance may be obtained by selecting resistant
5 marker types for any two of the three resistance loci (Fig. 2).

Given that PI437654, Peking, and PI90763 have the same resistance loci for SCN race-3, markers linked to these loci should be useful for marker-assisted selection
10 in germplasm related to these sources, and other sources that are shown to have the same resistance loci. However, PI88788, another common source of SCN race-3 resistance, lacks a resistance allele at either G or M and has a resistance allele at a different locus than
15 does Peking (Rao-Arelli, et al., Crop Sci. 32:862-864, 1992) and PI437654. That unique resistance locus can be genetically mapped to identify the necessary markers for marker-assisted selection of all three SCN race-3 resistance loci in populations related to PI88788.

20

EXAMPLE 2

RAPD PROTOCOL AND MARKERS

In using RAPD technology for mapping SCN resistance loci, the following markers were utilized:

	Public Primer Name	Linkage Group	Primer Sequence	Mapped Fragment Sizes (kb)
	UBC440	G	CTG TCG AAC C	0.38;N*
10	UBC379	M	GGG CTA GGG T	0.50;N
	OPC-04	M	CCG CAT CTA C	1.05;N

*N means "null" or no fragment

15

The following procedure was followed for performing RAPD mapping:

RAPD PROTOCOL

20 1. Thaw primers, DNA templates, 10X buffers, MgCl₂, dNTPs

2. Amplification reaction mix (25ml reaction):

25	Reagent	Stock Conc.	Reaction Conc.	Reaction Vol.
	MgCl ₂	25 mM	4 mM	4 ml
	dNTP	1 mM	0.2 mM	5 ml
	Buffer	10X	1X	2.5 ml
30	Enzyme	10 units/ml	2.5 units	0.25 ml
	H ₂ O (HPLC grade)			
	Primer	2 mM	0.2 mM	2.5 ml
	DNA Template	12.5 ng/ml	1 ng/ml	2 ml

35 3. Add DNA template or primer to eppendorph tubes or 96-well PCR plate. (It is important not to add both the template and primer to the reaction mix.)

4. Make reaction mix (MgCl₂, dNTP, buffer, H₂O, primer or template) and mix well.

40 5. Add enzyme (Stoeffel Fragment) to reaction mix and mix gently.

6. Add master mix to eppendorph tubes or PCR plate.

7. Add one drop light mineral oil to reach reaction, cover and place in thermal cycler.

8. Thermal Cycler program (45 cycles)
 - 94°C 1 min
 - 36°C 1 min
 - 36°C-->72°C ramp 1°C/2 sec
 - 5 72°C 2 min
9. After amplification add 4 ml loading buffer to each reaction.
10. Load 12.5 ul of each reaction into wells of an agarose gel (100ml gel 2.0% NuSieve 3:1 agarose; 0.1M TAE). Load 123bp size standard along with samples. Electrophorese for 180 volt-hours.

Although the foregoing invention has been described in detail for purposes of clarity and understanding, it will be clear to those skilled in the art that certain modifications may be practiced within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. A method of reliably and predictably introgressing soybean cyst nematode resistance into non-resistant soybean germplasm comprising using one or more nucleic acid markers for marker assisted selection among soybean lines to be used in a soybean breeding program, wherein the nucleic acid markers are pA85a, php02302a, php02340a, pk400a, pt155a, pBLT24a, php05180a, pSAC3a, pA1116, php02366a, php02361a, UBC440a, pk69a, pL50b, pA226a, pA715a, pk24a, pB157b, php02275a, UBC379a, OPC-04a, or php02301a.
2. The method of Claim 1 wherein the source of soybean cyst nematode resistance is PI437654 or a descendant thereof.
3. The method of Claim 1 wherein the source of soybean cyst nematode resistance is Peking or a descendant thereof.
4. The method of Claim 1 wherein the source of soybean cyst nematode resistance is PI90763 or a descendant thereof.
5. The method of Claim 1 wherein the marker assisted selection comprises the use of restriction fragment length polymorphism analysis.
6. The method of Claim 1 wherein the marker assisted selection comprises the use of RAPD analysis.
7. The method of Claim 1 wherein the marker assisted selection comprises the use of microsatellite analysis.
8. A quantitative trait locus associated with resistance to soybean cyst nematode race-3, said locus mapped using one or more nucleic acid markers.

9. The quantitative trait locus of Claim 8, said locus mapping to soybean linkage group A, and mapped by one or more of markers pA85a, php02302a, php02340a, pk400a, pT155a, pBLT24b, php05180a, pSAC3a, and pA111b.
- 5
10. The quantitative trait locus of Claim 8, said locus mapping to soybean linkage group G, and mapped by one or more of markers php02366a, php02361a, UBC440a, pk69a, UBC576a, and pL50b.
- 10
11. The quantitative trait locus of Claim 8, said locus mapping to soybean linkage group M, and mapped by one or more of markers pA226a, pA715a, pk24a, pB157b, php02275a, UBC379a, OPC-04a, and php02301a.
- 15
12. A race-3 soybean cyst nematode resistant soybean line developed using the method of Claim 1.
- 20
13. A race-3 soybean cyst nematode resistant soybean line developed through the identification of parental lines possessing one or more of the quantitative trait loci of Claims 8, 9, 10, or 11.
- 25
14. A race-3 soybean cyst nematode resistant soybean line developed as part of a breeding program and possessing one or more of the quantitative trait loci of Claims 8, 9, 10, or 11.

